

# Hreinn Stefansson

## List of Publications by Year in descending order

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116  
papers

41,926  
citations

18482

62  
h-index

18130

120  
g-index

130  
all docs

130  
docs citations

130  
times ranked

41098  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
2	Variant of <i>TREM2</i> Associated with the Risk of Alzheimer's Disease. <i>New England Journal of Medicine</i> , 2013, 368, 107-116.	27.0	2,085
3	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. <i>Nature Genetics</i> , 2011, 43, 429-435.	21.4	1,708
4	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. <i>Nature Genetics</i> , 2014, 46, 989-993.	21.4	1,685
5	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. <i>Nature Genetics</i> , 2019, 51, 404-413.	21.4	1,625
6	Large recurrent microdeletions associated with schizophrenia. <i>Nature</i> , 2008, 455, 232-236.	27.8	1,619
7	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. <i>Nature Genetics</i> , 2019, 51, 63-75.	21.4	1,594
8	Common variants conferring risk of schizophrenia. <i>Nature</i> , 2009, 460, 744-747.	27.8	1,572
9	Neuregulin 1 and Susceptibility to Schizophrenia. <i>American Journal of Human Genetics</i> , 2002, 71, 877-892.	6.2	1,550
10	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	21.4	1,538
11	Association between Microdeletion and Microduplication at 16p11.2 and Autism. <i>New England Journal of Medicine</i> , 2008, 358, 667-675.	27.0	1,476
12	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. <i>Nature</i> , 2008, 452, 638-642.	27.8	1,399
13	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	21.4	1,395
14	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018, 50, 381-389.	21.4	1,332
15	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	21.4	1,307
16	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191
17	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.2	1,098
18	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. <i>Cell</i> , 2019, 179, 1469-1482.e11.	28.9	935

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19	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
20	A common inversion under selection in Europeans. <i>Nature Genetics</i> , 2005, 37, 129-137.	21.4	747
21	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	21.4	629
22	CNVs conferring risk of autism or schizophrenia affect cognition in controls. <i>Nature</i> , 2014, 505, 361-366.	27.8	588
23	A Genetic Risk Factor for Periodic Limb Movements in Sleep. <i>New England Journal of Medicine</i> , 2007, 357, 639-647.	27.0	582
24	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , 2016, 48, 856-866.	21.4	520
25	Association of Neuregulin 1 with Schizophrenia Confirmed in a Scottish Population. <i>American Journal of Human Genetics</i> , 2003, 72, 83-87.	6.2	518
26	Rare chromosomal deletions and duplications in attention-deficit hyperactivity disorder: a genome-wide analysis. <i>Lancet, The</i> , 2010, 376, 1401-1408.	13.7	485
27	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease. <i>Nature Genetics</i> , 2021, 53, 1276-1282.	21.4	430
28	Disruption of the neurexin 1 gene is associated with schizophrenia. <i>Human Molecular Genetics</i> , 2009, 18, 988-996.	2.9	424
29	Detection of sharing by descent, long-range phasing and haplotype imputation. <i>Nature Genetics</i> , 2008, 40, 1068-1075.	21.4	409
30	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. <i>Nature</i> , 2011, 478, 97-102.	27.8	394
31	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. <i>Nature Neuroscience</i> , 2015, 18, 953-955.	14.8	351
32	Large-scale integration of the plasma proteome with genetics and disease. <i>Nature Genetics</i> , 2021, 53, 1712-1721.	21.4	340
33	Genome-wide meta-analysis identifies new susceptibility loci for migraine. <i>Nature Genetics</i> , 2013, 45, 912-917.	21.4	338
34	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. <i>Nature Genetics</i> , 2010, 42, 869-873.	21.4	332
35	Excessive burden of lysosomal storage disorder gene variants in Parkinson's disease. <i>Brain</i> , 2017, 140, 3191-3203.	7.6	323
36	Mapping of a familial essential tremor gene, FET1, to chromosome 3q13. <i>Nature Genetics</i> , 1997, 17, 84-87.	21.4	288

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37	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. <i>Nature Genetics</i> , 2015, 47, 445-447.	21.4	283
38	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. <i>Nature Genetics</i> , 2017, 49, 1584-1592.	21.4	248
39	Brain age prediction using deep learning uncovers associated sequence variants. <i>Nature Communications</i> , 2019, 10, 5409.	12.8	238
40	Copy number variations of chromosome 16p13.1 region associated with schizophrenia. <i>Molecular Psychiatry</i> , 2011, 16, 17-25.	7.9	227
41	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. <i>Human Molecular Genetics</i> , 2014, 23, 4420-4432.	2.9	227
42	Identification of a large set of rare complete human knockouts. <i>Nature Genetics</i> , 2015, 47, 448-452.	21.4	214
43	Variant in the sequence of the LINGO1 gene confers risk of essential tremor. <i>Nature Genetics</i> , 2009, 41, 277-279.	21.4	211
44	Genetic factors contribute to the risk of developing endometriosis. <i>Human Reproduction</i> , 2002, 17, 555-559.	0.9	192
45	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. <i>Human Molecular Genetics</i> , 2012, 21, 4996-5009.	2.9	176
46	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2017, 81, 325-335.	1.3	175
47	Identification of a novel neuregulin 1 at-risk haplotype in Han schizophrenia Chinese patients, but no association with the Icelandic/Scottish risk haplotype. <i>Molecular Psychiatry</i> , 2004, 9, 698-704.	7.9	149
48	Selection against variants in the genome associated with educational attainment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E727-E732.	7.1	149
49	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. <i>Circulation</i> , 2015, 131, 2061-2069.	1.6	145
50	Deletion of TOP3 <sup>1</sup> , a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. <i>Nature Neuroscience</i> , 2013, 16, 1228-1237.	14.8	144
51	A genome-wide scan for preeclampsia in the Netherlands. <i>European Journal of Human Genetics</i> , 2001, 9, 758-764.	2.8	140
52	Multiple novel transcription initiation sites for NRG1. <i>Gene</i> , 2004, 342, 97-105.	2.2	139
53	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. <i>Nature Genetics</i> , 2022, 54, 152-160.	21.4	135
54	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. <i>Human Molecular Genetics</i> , 2013, 22, 1039-1049.	2.9	122

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55	Neuregulin 1 and schizophrenia. <i>Annals of Medicine</i> , 2004, 36, 62-71.	3.8	119
56	A Mouse Model that Recapitulates Cardinal Features of the 15q13.3 Microdeletion Syndrome Including Schizophrenia- and Epilepsy-Related Alterations. <i>Biological Psychiatry</i> , 2014, 76, 128-137.	1.3	95
57	Genome-wide association study implicates CHRNA2 in cannabis use disorder. <i>Nature Neuroscience</i> , 2019, 22, 1066-1074.	14.8	94
58	Shared genetic basis for migraine and ischemic stroke. <i>Neurology</i> , 2015, 84, 2132-2145.	1.1	91
59	Polygenic risk scores for schizophrenia and bipolar disorder associate with addiction. <i>Addiction Biology</i> , 2018, 23, 485-492.	2.6	90
60	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. <i>American Journal of Human Genetics</i> , 2016, 98, 898-908.	6.2	89
61	Common variant at 16p11.2 conferring risk of psychosis. <i>Molecular Psychiatry</i> , 2014, 19, 108-114.	7.9	85
62	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	12.0	79
63	Genome-wide common and rare variant analysis provides novel insights into clozapine-associated neutropenia. <i>Molecular Psychiatry</i> , 2017, 22, 1502-1508.	7.9	75
64	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. <i>Translational Psychiatry</i> , 2019, 9, 258.	4.8	75
65	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. <i>Communications Biology</i> , 2021, 4, 156.	4.4	72
66	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. <i>Translational Psychiatry</i> , 2017, 7, e1109-e1109.	4.8	67
67	Truncating mutations in RBM12 are associated with psychosis. <i>Nature Genetics</i> , 2017, 49, 1251-1254.	21.4	63
68	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. <i>Neuron</i> , 2018, 98, 743-753.e4.	8.1	63
69	Genome-Wide Analysis Shows Increased Frequency of Copy Number Variation Deletions in Dutch Schizophrenia Patients. <i>Biological Psychiatry</i> , 2011, 70, 655-662.	1.3	61
70	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , 2020, 41, 2618-2628.	2.2	61
71	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. <i>Molecular Psychiatry</i> , 2021, 26, 4179-4190.	7.9	58
72	Convergent lines of evidence support CAMKK2 as a schizophrenia susceptibility gene. <i>Molecular Psychiatry</i> , 2014, 19, 774-783.	7.9	56

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73	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. <i>JAMA Psychiatry</i> , 2020, 77, 420.	11.0	54
74	GBA and APOE $\epsilon$ 4 associate with sporadic dementia with Lewy bodies in European genome wide association study. <i>Scientific Reports</i> , 2019, 9, 7013.	3.3	53
75	Parental Origin of Interstitial Duplications at 15q11.2-q13.3 in Schizophrenia and Neurodevelopmental Disorders. <i>PLoS Genetics</i> , 2016, 12, e1005993.	3.5	51
76	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. <i>Molecular Psychiatry</i> , 2020, 25, 584-602.	7.9	49
77	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. <i>Nature Communications</i> , 2020, 11, 3368.	12.8	49
78	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. <i>Nature Communications</i> , 2017, 8, 14265.	12.8	48
79	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. <i>Cephalalgia</i> , 2016, 36, 648-657.	3.9	47
80	Meta-analysis of Alzheimer's disease on 9,751 samples from Norway and IGAP study identifies four risk loci. <i>Scientific Reports</i> , 2018, 8, 18088.	3.3	47
81	Association of AADAC Deletion and Gilles de la Tourette Syndrome in a Large European Cohort. <i>Biological Psychiatry</i> , 2016, 79, 383-391.	1.3	41
82	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. <i>Communications Biology</i> , 2020, 3, 703.	4.4	40
83	Neuregulin 1 in schizophrenia: out of Iceland. <i>Molecular Psychiatry</i> , 2003, 8, 639-640.	7.9	36
84	The influence of genetic constitution on migraine drug responses. <i>Cephalalgia</i> , 2016, 36, 624-639.	3.9	34
85	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , 2020, 49, 1022-1031.	1.9	34
86	The Adult Reading History Questionnaire (ARHQ) in Icelandic. <i>Journal of Learning Disabilities</i> , 2014, 47, 532-542.	2.2	33
87	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. <i>Cephalalgia</i> , 2015, 35, 489-499.	3.9	32
88	Identification of genetic overlap and novel risk loci for attention-deficit/hyperactivity disorder and bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 4055-4065.	7.9	31
89	Identifying the Common Genetic Basis of Antidepressant Response. <i>Biological Psychiatry Global Open Science</i> , 2022, 2, 115-126.	2.2	31
90	Reproductive fitness and genetic risk of psychiatric disorders in the general population. <i>Nature Communications</i> , 2017, 8, 15833.	12.8	30

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91	Effects of copy number variations on brain structure and risk for psychiatric illness: Large-scale studies from the ENIGMA working groups on CNVs. <i>Human Brain Mapping</i> , 2022, 43, 300-328.	3.6	30
92	Reciprocal White Matter Changes Associated With Copy Number Variation at 15q11.2 BP1-BP2: A Diffusion Tensor Imaging Study. <i>Biological Psychiatry</i> , 2019, 85, 563-572.	1.3	29
93	Multimomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1085-1095.	0.9	26
94	Endometriosis is not associated with or linked to the GALT gene. <i>Fertility and Sterility</i> , 2001, 76, 1019-1022.	1.0	24
95	The association between candidate migraine susceptibility loci and severe migraine phenotype in a clinical sample. <i>Cephalalgia</i> , 2016, 36, 615-623.	3.9	24
96	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. <i>Translational Psychiatry</i> , 2021, 11, 182.	4.8	24
97	Data Resource Profile: The Copenhagen Hospital Biobank (CHB). <i>International Journal of Epidemiology</i> , 2021, 50, 719-720e.	1.9	23
98	Addictions and their familiarity in Iceland. <i>Annals of the New York Academy of Sciences</i> , 2010, 1187, 208-217.	3.8	22
99	Roadmap for a precision-medicine initiative in the Nordic region. <i>Nature Genetics</i> , 2019, 51, 924-930.	21.4	22
100	MAP1B mutations cause intellectual disability and extensive white matter deficit. <i>Nature Communications</i> , 2018, 9, 3456.	12.8	21
101	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. <i>Nature Communications</i> , 2022, 13, 634.	12.8	21
102	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. <i>Current Biology</i> , 2020, 30, 4643-4653.e3.	3.9	19
103	Identification of Genetic Loci Shared Between Attention-Deficit/Hyperactivity Disorder, Intelligence, and Educational Attainment. <i>Biological Psychiatry</i> , 2020, 87, 1052-1062.	1.3	13
104	Comparing migraine with and without aura to healthy controls using RNA sequencing. <i>Cephalalgia</i> , 2019, 39, 1435-1444.	3.9	12
105	HLA-DQB1 6672G>C (rs113332494) is associated with clozapine-induced neutropenia and agranulocytosis in individuals of European ancestry. <i>Translational Psychiatry</i> , 2021, 11, 214.	4.8	12
106	Predicting facial characteristics from complex polygenic variations. <i>Forensic Science International: Genetics</i> , 2015, 19, 263-268.	3.1	11
107	Analysis of Diffusion Tensor Imaging Data From the UK Biobank Confirms Dosage Effect of 15q11.2 Copy Number Variation on White Matter and Shows Association With Cognition. <i>Biological Psychiatry</i> , 2021, 90, 307-316.	1.3	11
108	Predicting the probability of death using proteomics. <i>Communications Biology</i> , 2021, 4, 758.	4.4	10

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109	Neuroimaging findings in neurodevelopmental copy number variants: identifying molecular pathways to convergent phenotypes. <i>Biological Psychiatry</i> , 2022, , .	1.3	9
110	Elevated common variant genetic risk for tourette syndrome in a densely-affected pedigree. <i>Molecular Psychiatry</i> , 2021, 26, 7522-7529.	7.9	8
111	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. <i>Nature Communications</i> , 2022, 13, 1598.	12.8	8
112	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. <i>Nature Communications</i> , 2019, 10, 1777.	12.8	7
113	Cohort profile: Copenhagen Hospital Biobank - Cardiovascular Disease Cohort (CHB-CVDC): Construction of a large-scale genetic cohort to facilitate a better understanding of heart diseases. <i>BMJ Open</i> , 2021, 11, e049709.	1.9	7
114	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. <i>Human Molecular Genetics</i> , 2013, 22, 1696-1696.	2.9	3
115	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. <i>Intelligence</i> , 2021, 88, 101565.	3.0	2
116	Cognition in Schizophrenia. <i>Biological Psychiatry</i> , 2021, 90, 4-5.	1.3	0